1/7

71.3% identity in 376 nt overlap; init: 76, opt: 608

```
10
              20
                   30
                          40
                                50
                                     60
_bgdf cttgggagaactagtgaggaacatatttctccatgccagtcctcttcctaaaggcagga
       10
             20
                   30
                         40
                               50
       70
              80
                    90
                            100
.. ...
         _ hgdp agagectagettggtetettaaataaattteaggtgtgtgggtggaetaeggtetettet
             80
                   90
                        100
                            110
                                   120
                           CATA-1
                                       E-Box
   120
               140
                     150
                           160
                                 170
_ hgdf gtaatcaggcctcaagtatgcctagctgaagatt----TTATCAgctctatatcaagca
       130
           140
                   150
                                  170
         190
                200
                      210
                            220
                                  230
_ mgdf gctgacaacacggt+tttatccaatttgttctcattagatacacgttta<u>tctactta</u>ttt
    _ bodf cotortacecotrittingocartitgt--tarteachickchittacetggitatit
                       210
                             220
          190
                200
    180
                                   230
    240
                      270
                            280
          250
                260
                                  290
THEOP GET TOTTTOCCTOTTTCTCCTGACATTTATTCAAACCACCACGAGTATCGTCACCCT
    #:::## If ## ### #### ##### # ######
_ hode accitic-cictet-titiccctgg-cattiacgtalaaccc----Gitactgttacact
     240
            250
                   260
                        270
                      330
                            340
                                  350
    300
          310
                320
_ bgdp accognetalctatgtagctglaagtctalgatalattglagglatgatcttalatalaat
   290
         300
               310
                     320
                           330
    360
          370
_ mgdf crcttagggcrgaga (SEQ IN NO: 2)
    _ hgdp crcrcatititigaga (SEQ ID NO: 3)
   350
         360
```

Figure 1



